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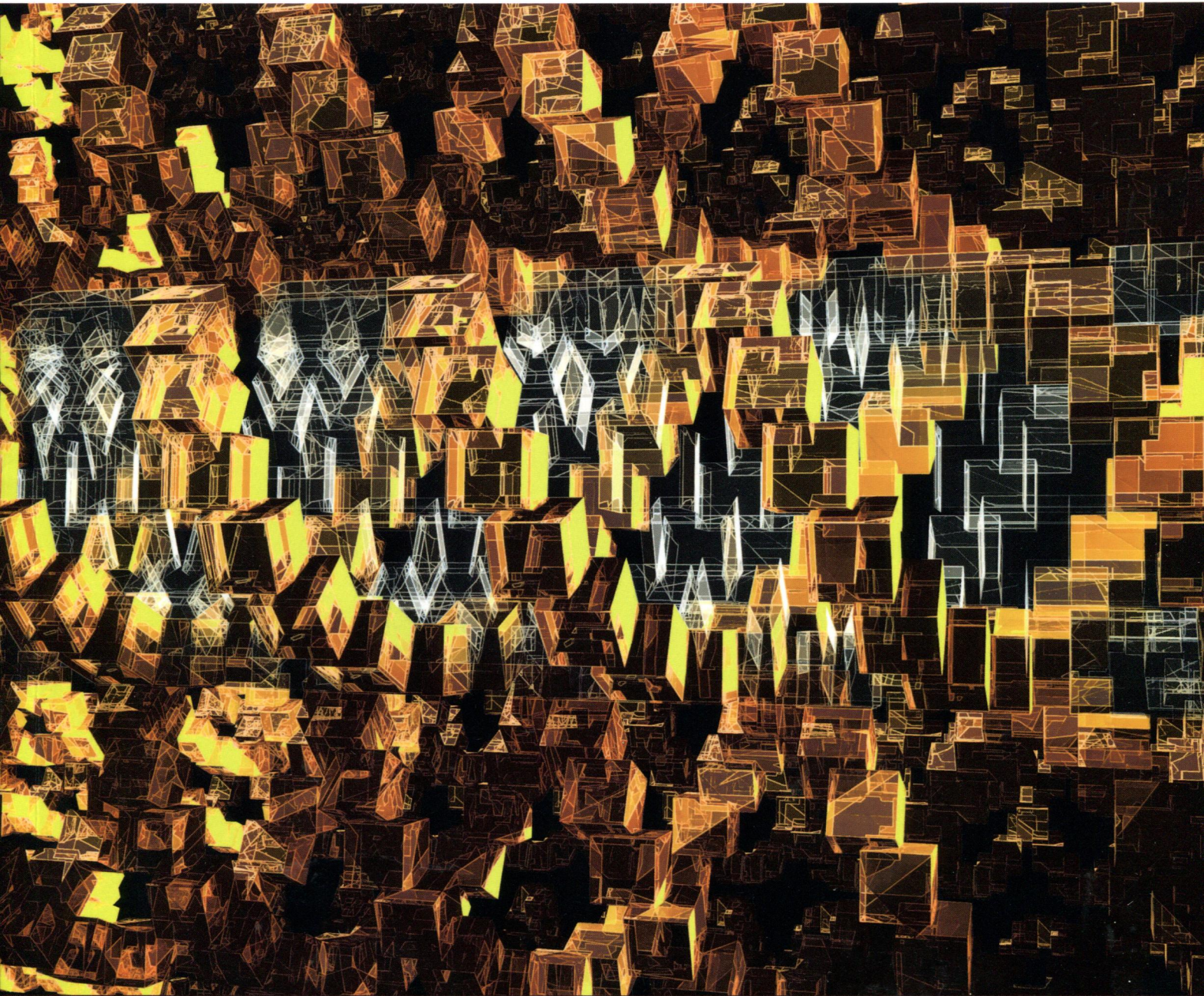
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## REVIEWS

december 2014 volume 15 no. 12  
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# GENETICS

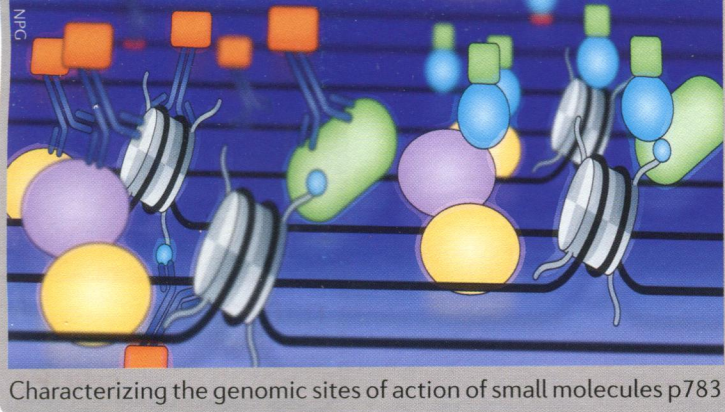


### ZOOMING TO HIGH DETAIL

Interrogating the epigenome at  
base-pair resolution

### Holding on to be counted

A census of human RNA-binding  
proteins



Characterizing the genomic sites of action of small molecules p783

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## REVIEWS

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FEATURED  
ARTICLE



### Unravelling the genomic targets of small molecules using high-throughput sequencing

*Raphaël Rodriguez and Kyle M. Miller*

Various small molecules, including numerous anticancer agents, act by targeting DNA or protein components of chromatin. This Review describes how various complementary technologies use high-throughput sequencing to delineate drug responses, from identifying the genomic binding sites of drugs or their targets, to the ensuing changes to chromatin states and gene expression. These insights should facilitate the rational use of these therapies.

797

### Microbial genome-enabled insights into plant-microorganism interactions

*David S. Guttman, Alice C. McHardy and Paul Schulze-Lefert*

Various bacterial and eukaryotic microorganisms engage in interactions with plant hosts, ranging from co-evolutionary arms races between phytopathogens and their hosts to the beneficial effects of mutualistic microorganisms. This Review discusses how next-generation sequencing of microbial isolates and environmental samples has provided insights into the mechanisms and genome-wide evolution of pathogenesis in phytopathogens, as well as a more global understanding of plant-associated microbial communities.

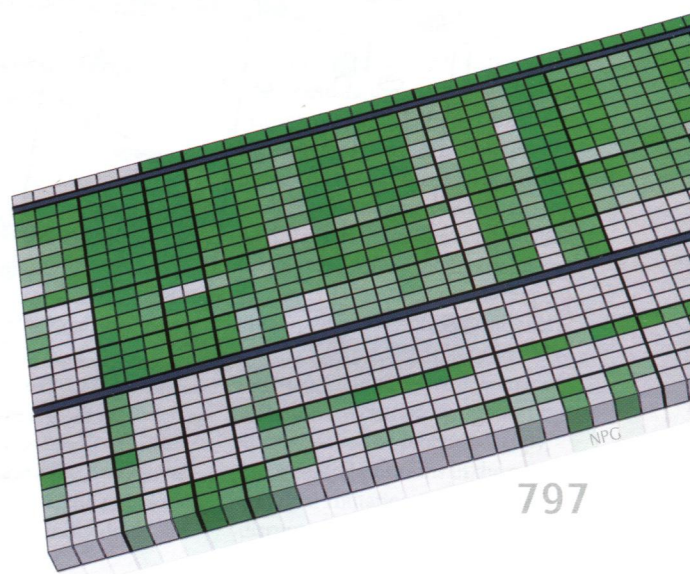
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### High-resolution digital profiling of the epigenome

*Gabriel E. Zentner and Steven Henikoff*

The resolution of epigenomic profiling has been vastly augmented with the adoption of new approaches to interrogate varied features of the epigenome. This Review describes these techniques and outlines the ways in which these genome-wide tools can be used to examine the epigenome.



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*Paul G. Higgs and Niles Lehman*

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*Doug Speed and David J. Balding*

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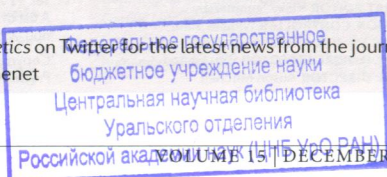
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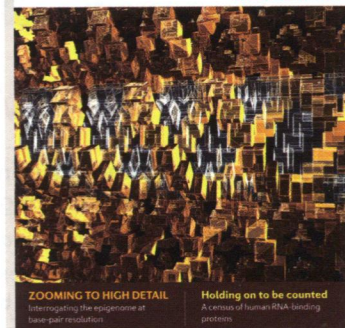


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**GENETICS**



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**Holding on to be counted**

A census of human RNA-binding proteins

► **COVER:** 'Discern' by Patrick Morgan.

## RESEARCH HIGHLIGHTS

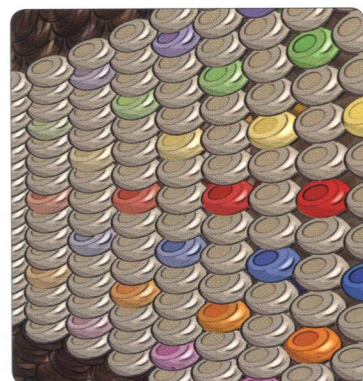
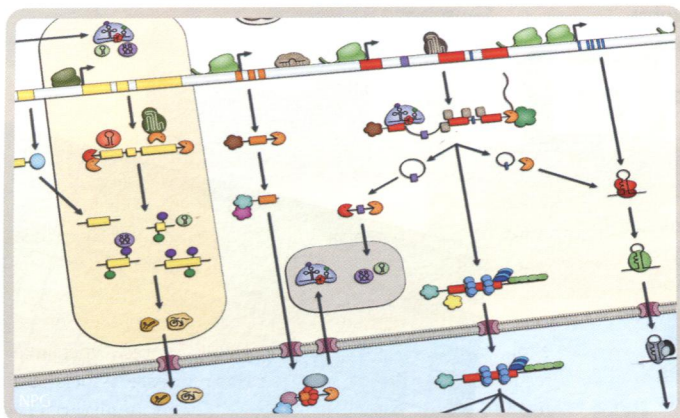
777 Selections from the recent scientific literature

## ANALYSIS

829 **A census of human RNA-binding proteins**

*Stefanie Gerstberger, Markus Hafner and Thomas Tuschl*

Analyses of post-transcriptional gene regulation and the protein factors involved have been substantially driven forward by technological advances such as next-generation sequencing and modern protein mass spectrometry. This Analysis provides a census of 1,542 manually curated RNA-binding proteins, for which the authors have investigated interactions with different classes of RNA, evolutionary conservation, abundance and tissue-specific expression.



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